```
m3-OST-1  MTLLLLGAVL LVAQPQLVHS HPAAPGPGLK QQELLRKVII   40
h3-OST-1  MAALLLGAVL LVAQPQLVPS RPA----ELG QQELLRKAGT   36

m3-OST-1  LPEDTGEGTA SNGSTQQLPQ TIIIGVRKGG TRALLEMLSL   80
h3-OST-1  LQDDVRDGVA PNGSAQQLPQ TIIIGVRKGG TRALLEMLSL   76

m3-OST-1  HPDVAAAENE VHFFDWEEHY SQGLGWYLTQ MPFSSPHQLT  120
h3-OST-1  HPDVAAAENE VHFFDWEEHY SHGLGWYLSQ MPFSWPHQLT  116

m3-OST-1  VEKTPAYFTS PKVPERIHSM NPTIRLLLIL RDPSERVLSD  160
h3-OST-1  VEKTPAYFTS PKVPERVYSM NPSIRLLLIL RDPSERVLSD  156

m3-OST-1  YTQVLYNHLQ KHKPYPPIED LLMRDGRLNL DYKALNRSLY  200
h3-OST-1  YTQVFYNHMQ KHKPYPSIEE FLVRDGRLNV DYKALNRSLY  196

m3-OST-1  HAHMLNWLRF FPLGHIHIVD GDRLIRDPFP EIQKVERFLK  240
h3-OST-1  HVHMQNWLRF FPLRHIHIVD GDRLIRDPFP EIQKVERFLK  236

m3-OST-1  LSPQINASNF YFNKTKGFYC LRDSGKDRCL HESKGRAHPQ  280
h3-OST-1  LSPQINASNF YFNKTKGFYC LRDSGRDRCL HESKGRAHPQ  276

m3-OST-1  VDPKLLDKLH EYFHEPNKKF FKLVGRTFDW H           311
h3-OST-1  VDPKLLNKLH EYFHEPNKKF FELVGRTFDW H           307
```

Figure 1


599 KTCDRFPKLLIIGPQKTGTTALYLFLGMHPDLSSNYPSSETFEEIQFFN GHNYHKGIDWYMEFFPIPSNTTSDFYFEKS NST-1
598 KTCDRLPKFLIVGPQKTGTTAIHFFLSLHPAVTSSFPSPSTFEEIQFFN SPNYHKGIDWYMDFFPVPSNASTDFLFEKS NST-2
23 TSKKRFPDAIIVGVKKSGTRALLEFLRVNPLI KAPGPEVHFFDKNFN KGLEWYREQMPETKFGEV TIEKS ce3-OST
193 GEKK LPQALIIGVKKGGTRALLEAIRVHPDV RAVGVEPHFFDRN YEKGLEWYRNVMPKTLD GQITMEKT 3-OST-4
148 GS KQLPQAIIIGVKKGGTRALLEFLRVHPDV RAVGAEPHFFDRS YDKGLAWYRDLMPRTLD GQITMEKT 3-OST-3A
110 GT KRLPQALIVGVKKGGTRAVLEFIRVHPDV RALGTEPHFFDRN YGRGLDWYRSLMPRTLE SQITLEKT 3-OST-2
49 GSAQQLPQTIIIGVRKGGTRALLEMLSLHPDV AAAENEVHFFDWEEHYSHGLGWYLSQMPFSWP HQLTVEKT 3-OST-1
678 ANYFDSEVAPRRAAALLPKAKVLTILINPADRAYSWYQHQRAHDDPVALKYTFHEVITAGSDA SSKLRALQ NST-1
677 ATYFDSEVVPRRGAALLPRAKIITVLTNPADRAYSWYQHQRAHGDPVALNYTFYQVISASSQT PLALRSLQ NST-2
93 PAYFHSKMAPERIKSLNPNTKIIIVVRDPVTRAISDYTQSSSKRKRVGLM PSFETMAVGNCANWLRTNCTTKTRGVNAG ce3-OST
262 PSYFVTNEAPKRIHSMAKDIKLIVVVRNPVTRAISDYTQT LSKKPEIPTFEVLAFKNRT LGLIDAS 3-OST-4
217 PSYFVTREAPARISAMSKDTKLIVVVRDPVTRAISDYTQT LSKRPDIPTFESLTFKNRT AGLIDTS 3-OST-3A
179 PSYFVTQEAPRRIFNMSRDTKLIVVVRNPVTRAISDYTQT LSKKPDIPTFEGLSFRNRT LGLVDVS 3-OST-2
121 PAYFTSPKVPERVYSMNPSIRLLLILRDPSERVLSDYTQVFYNHMQKHKPYPSIEEFLVRD GRLNVD 3-OST-1
749 NRCLVPGWYATHIERWLSAYHANQILVLDGKLLRTEPAKVMDMVQKFLGVTNTIDYHKTLAFDPKKGFWC QLLEGGKT NST-1
748 NRCLVPGYYSTHLQRWLTYYPSGQLLIVDGQELRTNPAASMESIQKFLGITPFLNYTRTLRFDDDKGFWC QGLEGGKT NST-2
172 WGAIRIGVYHKHMKRWLDHFPIENIHIVDGEKLISNPADEISATEKFLGLKPVAK PEKFGVDPIKKFPCIK NEDGKL ce3-OST
328 WSAIRIGIYALHLENWLQYFPLSQILFVSGERLIVDPAGEMAKVQDFLGLKRVVT KKHFYFNKTKGFPCLKKPEDSSAP 3-OST-4
283 WSAIQIGIYAKHLEHWLRHFPIRQMLFVSGERLISDPAGELGRVQDFLGLKRIIT DKHFYFNKTKGFPCLKKAEGSSRP 3-OST-3A
245 WNAIRIGMYVLHLESWLQYFPLAQIHFVSGERLITDPAGEMGRVQDFLGIKRFIT DKHFYFNKTKGFPCLKKTESSLLP 3-OST-2
188 YKALNRSLYHVHMQNWLRFFPLRHIHIVDGDRLIRDPFPEIQKVERFLKLSPQIN ASNFYFNKTKGFYCLR DSGRD 3-OST-1
827 KCLGKSKGRKYPEMDLDSRAFLKDYYRDHNIELSKLLYKMGQTLPTWLREDLQNTR NST-1
826 RCLGRSKGRRYPDMDTESRLFLTDFFRNHNLELSKLLSRLGQPVPSWLREELQHSSLG NST-2
249 HCLGKTKGRHHPDVEPSVLKTLREFYGPENKKFYQMINHWFDW ce3-OST
407 RCLGKSKGRTHPRIDPDVIHRLRKFYKPFNLMFYQMTGQDFQWEQEEGDK 3-OST-4
362 HCLGKTKGRTHPEIDREVVRRLREFYRPFNLKFYQMTGHDFGWDG 3-OST-3A
324 RCLGKSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE 3-OST-2
264 RCLHESKGRAHPQVDPKLLNKLHEYFHEPNKKFFELVGRTFDWH 3-OST-1

Figure 2

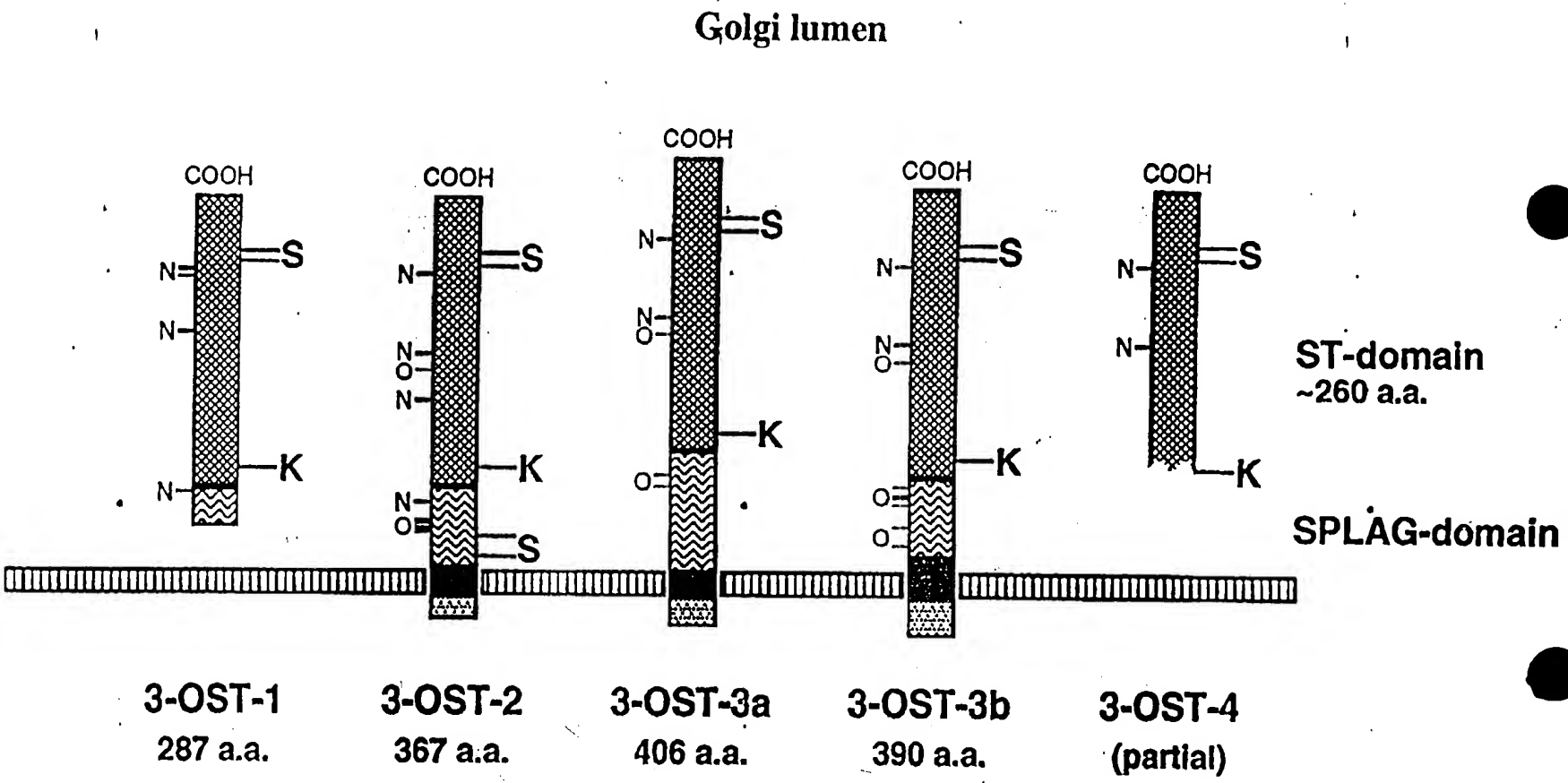
Golgi lumen
COOH
S
K
ST-domain
~260 a.a.
SPLAG-domain
3-OST-1
287 a.a.
3-OST-2
367 a.a.
3-OST-3a
406 a.a.
3-OST-3b
390 a.a.
3-OST-4
(partial)
Cytoplasm

FIGURE 3